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Copyright (c) 1993 - 2003 Compugen Ltd.
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Description	350512 Sequence 281308 Homo sap 262016 Homo sap 032736 Homo sap 284095 Homo sap	58163 Human D 50513 Sequenc 16894 Homo sa 533 Human alp 415 Human pla 652 Porcine a	79031 Rattus no 52372 Rat alpha 9030 Bos taurus 99377 Mouse alpha 113491 Mus musc 344975 Sequence 348495 Sequence 350528 Sequence 350528 Sequence 350528 Sequence 3648 Homo sapie	31000010000000000000000000000000000000	DNA linear PAT 06-FEB-2002 liata; Vertebrata; Euteleostomi; rrhini; Hominidae; Homo.
SUMMARIES	AX350512 AF281308 AF262016 AY032736 AF284095	AL158163 AX350513 AF316894 HUMADRA2 HUMADRA PIGA2AR	RU790 U790 U790 U790 11134 11134 3484 3484 3484 U726 U726	AK280399 AX350530 0 CPU25724 AF280400 E07358 HUMA2CIIA TRU345040 0 MUSALP2ADA 0 RATA2AR 0 RATA2BADR 0 RATA2BADR AC092603 AX350490 AK350489 AK350489 AK005900 HUMADRA2RA CVI315935 DVU04310	ALIGNMENTS 1350 bp ent WO0179561. 107 Chordata; Cran Primates; Cata 11, K.M. eceptor polymo 24 25-OCT-200
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Small.K.M., Forbes, S.L., Brown, K.M. and Liggett, S.B. An asn to lys polymorphism in the third intracellular human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling

J. Biol. Chem. 275 (49), 38518-38523 (2000)
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                  /note="compared to sequence
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hc

Liu, L. and Yuan, L.

Human alpha-2A adrenergic receptor gene and the genotype
nucleotide and motionsickness
Unpublished

Chases 1 to 3612)

Liu, L. and Yuan, L.

Direct Submission

Submitted (17-APR-2001) Key Laboratory of Molecular Bio
General Hospital of Airforce, Fucheng Road No. 30, Beij
China
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IYQIAKRRTRVPPSRRGPDAVAAPPGGTERRPNGLGPERSAGPGGAEAEPLPTQLNGA
PGEPAPAGPRDTDALDLEESSSSDHAERPPGPRREPREGFRGFRGKGKARASQVKFGDSLPR
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Homo sapiens.

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 3653)

Mao, Z.-M., Tang, K., Li, B.-M. and Jing, N.-H.

Cloning and expression of human alpha-2A adrenergic receptor in SY5Y cells

L Unpublished

E 2 (bases 1 to 3653)

Mao, Z.-M., Tang, K., Li, B.-M. and Jing, N.-H.

Direct Submission

AL Submitted (01-JUL-2000) Shanghai Institute of Physiology, Chinese Academy of Sciences, 320 Yue Yang Road, Shanghai 200031, P.R. China

Location/Qualifiers

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/Organism="Homo sapiens"
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P.R. China
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RGPGATGIGTPAAGPGGEERVGAAKASRWRGRQNREKRFTFVLAVUGVFVVCWFPFF
TYTLTAVGCSVPRTLFKFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKILCRGDRKRIV
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Direct Submission

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Submitted (13-DEC-2001) Wellcome Trust Sanger Institute, Hinx.c...,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

numquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

numquery@sanger.ac.uk

Clone version replaced gi:16944857.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

Where differences are found these are annotated as variations

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

corresponding to the overlapping clone, as we submit sequences with

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

chemistry or covered by high quality data (i.e., phred quality >=
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as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HgP/Chrl0 RP11-348N5 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm vECTOR: pBACe3.6 This sequence is the entire insert of clone RP11-348N5 The true left end of clone RP11-34921 is at 179266 in this sequence. The true right end of clone RP11-313D6 is at 44800 in this sequence.

Location/Qualifiers

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Small, K.M., Forbes, S.L., Brown, K.M. and Liggett, S.B. An asn to lys polymorphism in the third intracellular loop human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling J. Biol. Chem. 275 (49), 38518-38523 (2000)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(CE 1 (bases 1 to 3604)

Fraser, C.M., Arakawa, S., McCombie, W.R. and Venter, J.C.

Cloning, sequence analysis, and permanent expression of a human alpha 2-adrenergic receptor in Chinese hamster ovary cells.

Evidence for independent pathways of receptor coupling to adenylate cyclase attenuation and activation

AL J. Biol. Chem. 264 (20), 11754-11761 (1989)

B9308571

ED 2568356

Draft entry and computer-readable sequence for [1] kindly submitted by W.R.McCombie, 30-MAR-1989.
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                             / yence "alpha-2 adrenergic receptor old gene name 'ADRA2R'"
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Human platelet alpha-2-adrenergic receptor gene, complete
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M18415.1 GI:178191
alpha-2-adrenergic receptor; alpha-adrenergic receptor.
Human (lambda-EMBL 3 library) DNA.
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Human (lambda-EMBL 3 library) DNA.
SM Human (lambda-EMBL 3 library) DNA.
SM Human lia, Eutheria; Primates; Cararrhini; Hominidae; Homo.
E 1 (bases 1 to 1521)
S (cararrhini; Hominidae; Homo.
Caron, M.G., Lefkowitz, R.J. and Regan, J.W.
Cloning, sequencing, and expression of the gene coding for human platelet alpha 2-adrenergic receptor
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Science 238 (4827), 650-656 (1987)
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PIGAZAR

POCCINE alpha2A-adrenergic receptor (PORAZAR) gene, con J05652.

J05652.1 GI:164303

alpha-2A-adrenergic receptor.

Porcine liver DNA.

SM Sus scrofas

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus 1 (bases 1 to 1728)

Guyer, C.A., Horstman, D.A., Wilson, A.L., Clark, J.D., Kra and Limbird, L.E.

Unpublished (1990)

2 (bases 70 to 1582)

Guyer, C.A., Horstman, D.A., Wilson, A.L., Clark, J.D., Cra and Limbird, L.E.

Cloning, sequencing, and expression of the gene encodir porcine alpha 2-adrenergic receptor. Allosteric modulat H+, and amiloride analogs

J. Biol. Chem. 265 (28), 17307-17317 (1990)

SIT0371

Draft entry and computer-readable sequence for [J. Biol] (1990) In press] kindly submitted

by C.A.Guyer, 02-AUG-1990.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Fukaryota; Metazoa; Chordata; Hystricognathi; Caviidae; Cavia.

1 (bases 1 to 2291)

Svensson, S.P., Bailey, T.J., Porter, A.C., Richman, J.G. and Regan, J.W.

Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B, and alpha 2C adrenoceptor subtypes. Radioligand binding and functional coupling to a CAMP-responsive reporter gene Biochem. Pharmacol. 51 (3), 291-300 (1996)

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Direct Submission
Submitted (26-APR-1995) Jeremy G. Richma
Pharmacology and Toxicology, College of
AZ 85721, USA
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Structural, genetic and pharmacological identity of the restructural, genetic and pharmacological identity of the restartenergic receptor subtype cA2-47 and its molecular characterization in rat adrenal, adrenocortical carcinoma bovine retina
Mol. Cell. Biochem. 144 (2), 181-190 (1995)
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Molecular cloning, sequencing and expression of an alpha
2-adrenergic receptor complementary DNA from rat brain
Mol. Cell. Biochem. 97 (2), 161-172 (1990)
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Venkataraman, V., Duda, T.M. and Sharma, R.K.
Direct Submission
Submitted (20-NOV-1996) Cell Biology, UMDN
Dr., Stratford, NJ 08084, USA
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/codon_start=1
/product="alpha2D adrenergic receptor"
/product="alpha2D adrenergic receptor"
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SAVISFPPLISIEKKGAGGGQQPAEPSCKINDQKWYVISSSIGSFFAPCLIMILVYVR
IYQIAKRRTRVPPSRRGPDACSAPPGGADRRPNGLGPERGAGAGAEAEPLPTQLNGA
PGEPAPTRPRDGDALDLEESSSSEHAERPQGPGKPERGGRAKGKTKASQVKPGDSLPR
RGPGAAGPGASGSGQGEERAGGAKASRWRGRQNREKRFTFVLAVVIGVFVVCWFPFFF
TYTLIAVGCPVPYQLFNFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKILCRGDRKRIV
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strain="Sprague-Dawley"
db_xref="taxon:10116"
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Rat alpha-2-adrenergic receptor protein (RG20) gene, CM62372
M62372.1 GI:206615
alpha-2-adrenergic receptor; transmembrane protein.
Rattus norvegicus (strain Sprague-Dawley) adult liver
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="liver"
/dev_stage="adult"
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1 (bases 1 to 2923)

Venkataraman, V., Duda, T. and Sharma, R.K.

The bovine alpha 2D-adrenergic receptor gene: structure, expressicin retina, and pharmacological characterization of the encoded receptor

Mol. Cell. Biochem. 177 (1-2), 113-123 (1997)
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Venkataraman, V., Duda, T.M. and S
Direct Submission
Submitted (20-NOV-1996) Cell Bio
Stratford, NJ 08084, USA
Location/Qualifiers
1. .2923
/organism="Bos taurus"
/db_xref="taxon:9913"
1509. .2867
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Mol. Cell. Biochem. 177 (1-2),
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2 (bases 1 to 2923)
Venkataraman, V., Duda, T.M. and
Direct Submission
Submitted (20-NOV-1996) Cell B
Stratford, NJ 08084, USA
Location/Qualifiers
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db_xref="taxon:9913"
1509. .2867
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.

1 (bases 1 to 2923)

Venkataraman, V., Duda, T. and Sharma, R.K.

The bovine alpha 2D-adrenergic receptor gene: structure, expressit in retina, and pharmacological characterization of the encoded receptor
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7488. .7956
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8057. .9200
/note="assembly_fragment"
9301. .10747
/note="assembly_fragment"
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/note="assembly_fragment"
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FEATURES
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Sincent, B., Manthon, L., Lander, E., Ali, A., Allen, N., Andern, B., Birren, B., Lintcon, L., Wabbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boudhagleer, B., Chore, P., Colangalo, M., Colling, S., Collymone, A., Cook, A., Cooke, P., Parkellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhaupi, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyte, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyte, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyte, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyte, M., Gage, D., Galagan, J., Gardyna, S., Lander, M., Marthe, M., Kalls, C., Landergue, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Marthe, M., Match, M., Mat
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 204317)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-358H2
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Chemistry: Dye-terminator Big Dye; 100% of reads
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Center: Whitehead Institute/ MIT Center
Center code: WIBR
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have
                                                                                   * NOTE: This is a 'working draft' sequence. It currently
consists of 24 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
tof the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
the finished sequence as soon as it is available and
the accession number will be preserved.

This sequence will be preserved.

This sequence of 7387 bp in length

Take 100 bp.
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g of 3072 bp in length
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g of 3286 bp in length
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|db_xref="taxon:10090"
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15172: cont
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122788: cont:
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27175: cr
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12877: cont
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18061: cont
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30561: cont
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SAVISFPPLISIEKKGAGGGQQPAEPSCKINDQKWYVISSSIGSFFAPCLIMILVYVR
IYQIAKRRTRVPPSRRGPDACSAPPGGADRRPNGLGPERGAGTAGAEAEPLPTQLNGA
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TYTLIAVGCPVPYQLFNFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKILCRGDRKRIV
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Molecular cloning, sequencing and expression of an alpha
2-adrenergic receptor complementary DNA from rat brain
Mol. Cell. Biochem. 97 (2), 161-172 (1990)
91125329
2177834
2 (bases 1 to 1552)
Wypijewski, K., Duda, T. and Sharma, R.K.
Structural, genetic and pharmacological identity of the rat
2-adrenergic receptor subtype cA2-47 and its molecular
characterization in rat adrenal, adrenocortical carcinoma a
bovine retina
Mol. Cell. Biochem. 144 (2), 181-190 (1995)
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Venkataraman, V., Duda, T.M. and Sharma, R.K.
Direct Submission
Submitted (20-NOV-1996) Cell Biology, UMDN
Dr., Stratford, NJ 08084, USA
Location/Qualifiers
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Pred. No. 0.93;
0; Mismatches 4;
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                                                                                Score 34.6;
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Rattus norvegicus alpha2D
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nes 37; Conservative
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130. .1482
/note="alpha2A-adrenergic receptor (PORA2AR)"
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IYQIAKRRTRVPPSRRGGGGQQPAEPRCEINDQKWYVISSCIGSFFAPCLIMILVYVR
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RGPGAPAGGAPATGAGEERGGVAKASRWRGRQNREKRFTFVLAVVIGVFVVCWFPFFF
TYTLTAVGCSVPPTLFKFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKILCRGDRKRIV
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AC113491.3 GI:21327601
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
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Unpublished (1990)
2 (bases 70 to 1582)
Guyer, C.A., Horstman, D.A., Wilson, A.L., and Limbird, L.E.
Cloning, sequencing, and expression of porcine alpha 2-adrenergic receptor. Al H+, and amiloride analogs
J. Biol. Chem. 265 (28), 17307-17317 (19109167
2170371
Draft entry and computer-readable seque
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alpha2A-adrenergic receptor
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 1353)
Small, K.M., Forbes, S.L., Brown, K.M. and Liggett, S.B.
An asn to lys polymorphism in the third intracellular loop
human alpha 2A-adrenergic receptor imparts enhanced
agonist-promoted Gi coupling
J. Biol. Chem. 275 (49), 38518-38523 (2000)
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Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 25 25-OCT-2001;
Liggett, Stephen B. (US) ; Small, Kersten M.
Location/Qualifiers
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/ your / note = "G-protein coupled receptor" / codon start = 1 / codon start = 1 / codon start = 1 / product = "alpha 2A adrenergic receptor" / protein id = "AAK01634.1" / db xref = "GI:12698668" / translation = "MGSLQPDAGNASWNGTEAPGGGARATPYSLQVTLTLVCLAGLLM / LLTVFGNVLV1IAVFTSRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWYFG KAWCEIYLALDVLFCTSSIVHLCAISLDRYWSITQAIEYNLKRTPRRIKAIIITVWVI SAVISFPPLISIEKKGGGGGPQPAEPRCEINDQKWYVISSCIGSFFAPCLIMILVYVR IYQIAKRRTRVPPSRRGPDAVAAPPGGTERPFKGLGPERSAGPGGAEAEPLPTQLNGA PGEPAPAGPRDTDALDLEESSSSDHAERPPGPRRPERGFRGKGKARASQVKPGDSLPR RGPGATGIGTPAAGPGEERVGAAKASRWRGRQNREKRFTFVLAVVIGVFVVCWFPFFF TYTLTAVGCSVPRTLFKFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKILCRGDRKRIV
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Sciurognathi; Muridae; Murinae; Mus
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Sha 2-adrenergic receptor
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interspecies variation in
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/note="compared to wild type sequence p
Accession Number AF281308; polymorphic
Lys at amino acid 251"
/frequency="Caucasians 0.004; African-A/replace="c"
/replace="c"
/ 189 c 443 g 221 t
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Link, R., Daunt, D., Barsh, G., Chruscinski, A. Cloning of two mouse genes encoding alpha 2-cloning of two mouse genes encoding alpha 2-alpha 2-clo homolog responsible for an interantagonist binding
Mol. Pharmacol. 42 (1), 16-27 (1992)
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strain="129/Sv"
db_xref="taxon:10090"
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Mouse alpha-2 adrenergic recep
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M99377.1 GI:191882
alpha-2 adrenergic receptor.
Mus musculus (strain 129/Sv) D
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KAWCEIYLALDVLFCTSSIVHLCAISLDRYWSITQAIEYNLKRTPRRIKAIIITVWVI
SAVISFPPLISIEKKGGGGGPQPAEPRCEINDQKWYVISSCIGSFFAPCLIMILVYVR
IYQIAKRRTRVPPSRRGPDAVAAPPGGTERRPNGLGPERSAGPGGAEAEPLPTQLNGA
PGEPAPAGPRDTDALDLEESSSSDHAERPPGPRRPERGPRGKGRARASQVKPGDSLPR
RGPGATGIGTPAAGPGEERVGAAKASRWRGRQNREKRFTFVLAVVIGVFVVCWFPFFF
TYTLTAVGCSVPRTLFKFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKILCRGDRKRIV
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Eukaryota; Metazoa; Chordata; Liberaryota; Metazoa; Chordata; Catarrhini; Homiting Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Homiting Engages 1 to 3653)
S Mao, Z.-M., Tang, K., Li, B.-M. and Jing, N.-H.
Cloning and expression of human alpha-2A adrenergic receptor is yesy cells
Unpublished
SYSY cells
Loases 1 to 3653)
S Mao, Z.-M., Tang, K., Li, B.-M. and Jing, N.-H.
Direct Submission
AL Submitted (01-JUL-2000) Shanghai Institute of Physiology, Chi Academy of Sciences, 320 Yue Yang Road, Shanghai 200031, P.R.
Location/Qualifiers
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                                                                  /product="alpha-2A adrenergic receptor"
2085. .3437
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880. _2232
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Homo sapiens alpha-2A adrenergic
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/map="10q23-q25"
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<2085. .>3437
/gene="ADR2AR"
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Unrect Submissation

Submitted (13-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequestosanger.ac.uk

On Dec 5, 2001 this sequence version replaced gi:1694857.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either duuble-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT, Tr:, TREMBL; Wp:, WORNWEPP; Information on the WORNWEPP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 10, constructed by the Sanger Centre Chromosome 10
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This group
of Piecer de Jong. For further details see
http://www.chori.org/bacpac/home.htm
verices: Apple Apple
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|db_xref="taxon:9606"
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Mammalia; Eutheria; Primates;
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/db xref = "GI:9864782"
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                                                                                     Castellano, M., Giacche', M., Rossi, F., Rivadossi, F., Perani, Castellano, M., Giacche', M., Rossi, F., Rivadossi, F., Perani, Beschi, M. and Agabiti Rosei, E.

Direct Submission
Submitted (29-APR-2000) Medical and Surgical Sciences, Univolated (29-APR-2000) Medical and Surgical Sciences, Univolated (22-AUG-2000) Medical and Surgical Sciences, Univolated Update by Submitter

Sequence update by Submitter
On Aug 22, 2000 this sequence version replaced gi:9837145.
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Hom

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom

1 (bases 1 to 3604)

Fraser, C.M., Arakawa, S., McCombie, W.R. and Venter, J.C.

Cloning, sequence analysis, and permanent expression of alpha 2-adrenergic receptor in Chinese hamster ovary cell alpha 2-adrenergic receptor in Chinese hamster ovary cell evidence for independent pathways of receptor coupling to cyclase attenuation and activation

Gyclase attenuation and activation

J. Biol. Chem. 264 (20), 11754-11761 (1989)
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                                     alpha-2
Castellano, M., Giacche', M., Rossi, F., Rivadossi, F., Beschi, M. and Agabiti Rosei, E. A search for genetic variability in the human alphareceptor on chromosome 10 Unpublished
2 (bases 1 to 1941)
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Pred. No. 0.011;
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M23533
M23533.1 GI:178195
                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/map="10q24-q26"
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2078. 3430

2078. 3430

/gene="ZNF32"

2078. 3430

/gene="ZNF32"

/note="alpha-2 adrenergic receptor old gene name 'ADRA2R'"

/codon start=1

/protein id="AAA51665.1"

/db xref="G1:178196"

/db xref
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 3612)
Liu, L. and Yuan, L.
Human alpha-2A adrenergic receptor gene ar
nucleotide and motionsickness
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Lu. No. 0.0094;
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                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="10q23-q25"
1578. .1583
computer-readable 30-MAR-1989.
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1707. _1712
/note="glucocorticoid r
1723. _1728
/note="GRE related sequ
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Liu, L. and Yuan, L.
Direct Submission
Submitted (17-APR-2001) Key Lab
General Hospital of Airforce, F
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                                    .R.McCombie, 30-MAR-1989
Location/Qualifiers
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59. .1411
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/gene="ADRA2A"
/note="G-protein coupled receptor"
/codon_start=1
/product="alpha 2A adrenergic receptor"
/protein_id="AAF91441.1"
/b_xref="G1:9652210"
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LLTVFGNVLVIIAVFTSRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWYFG
KAWCEIYLALDVLFCTSSIVHLCAISLDRYWSITQAIEYNLKRTPRRIKAIIITVWVI
SAVISFPPLISIEKKGGGGGPQPAEPRCEINDQKWYVISSCIGSFFAPCLIMILVYVR
IYQIAKRRTRVPPSRRGPDAVAAPPGGTERRPNGLGPERSAGPGGAEAEPLPTQLNGA
PGEPAPAGPRDTDALDLEESSSSDHAERPPGPRRPFFFFVLAVVIGVFVVCWFPFFF
TYTLTAVGCSVPRTLFKFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKILCRGDRKRIV
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OH 45267, U
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; F (bases 1 to 1353)
Small, K.M., Forbes, S.L., Brown, K.M. and Liggett, S.B. An asn to lys polymorphism in the third intracellular human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling
J. Biol. Chem. 275 (49), 38518-38523 (2000)
                                                                                                             Length 1350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Liggett, S.B
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(ADRA2A)
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., suepnen B. (US); Small, Kersten M. (1
Location/Qualifiers
1. .1350
/organism="Homo sapiens"
/db_xref="taxon:9606"
a 490 c //1
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A Ave., Cincinnati,
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J. Biol. Chem.
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10948191
2 (bases 1 to 1353)
Small, K.M., Forbes, S.L., Bridges, K.M. an Direct Submission
Submitted (22-JUN-2000) Internal Medicir Cincinnati, 231 Bethesda Ave., Cincinnationalionalifiers
Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="10"
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/gene="ADRA2A"
<1. .>12:
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Kobilka, B.K., Matsui, H., Kobilka, T.S., Yang-1
Caron, M.G., Lefkowitz, R.J. and Regan, J.W.
Cloning, sequencing, and expression of the ge
human platelet alpha 2-adrenergic receptor
Science 238 (4827), 650-656 (1987)
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## ALIGNMENTS

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Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity, phosphorylation; inositol phosphate; alpha-2AAR; GenBank Accession AF281308; chromosome 10; ds.
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Best Local
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The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising;

(a) Obtaining a sample having a polymucleotide encoding an alpha-2B, alpha2A or alpha2C or fragment or comprising nucleotide positions 901-909

(b) detecting a polymorphic site comprising nucleotide positions 901-909

(c) detecting a polymorphic site comprising nucleotide positions 901-909

(d) detecting a polymorphic site comprising cytosine or guanine at positions 901-909

(e) detecting a polymorphic site comprising cytosine or guanine at positions 901-909

(f) a site comprising (A) (ggggcggggccg) or (B) (ggggcggctgag) at cypha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a sesociated with alpha2B, alpha2A or alpha2, comprising detecting addition, the technique may be used to predict an individual's response contral nervous system disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response combinations of these) or antagonist (e.g. vohimbine, prazosin, ARC 239, combinations of these) or antagonist (e.g. vohimbine, prazosin, ARC 239, crees) by detecting the polymorphic site and correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate correlated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis
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Pred. No. 0.00018;
0; Mismatches 1;
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ilarity 97.6%;
Conservative
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2000US-0636259.
2000US-0692077.
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SMALL K
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P-PSDB;
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
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rphism;
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gastrointestinal; cancer; central nervous system; cardiovascular gastrointestinal; respiratory system; single nucleotide polymorph. SNP; cell differentiation; ds.
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                                                                                                                                                                                                                                                                                                                                        Determining the degree of cytosine methylation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41
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                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
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ABQ47499 standard; DNA; 1733
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75.6%;
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2000DE-1044543
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05-SEP-2000;
                                                                 Homo sapiens
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligomerotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                              useful
of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                               Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA.
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13;
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Pred. No.
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75.6%;
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05-SEP-2000; 2000DE-1044543
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                                               WO200218632-A2
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Piepenbrock
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Kajkowski
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(SILV/)
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lcoholism;
ophrenia;
                                                                                                                                                                                             associated
sequences
sorders,
                                                                                                                                                                                           The present invention provides a number of human immune system associat genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       entia;
                                                                                                                                                 gene, ug
                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytostatic; antidepressant; neuroleptic; nootropic; antadrenergic alpha-1C-receptor; cytosine methylation; therapy; a behavioural disorder; neurological; psychiatric; cancer; schize Tourette's syndrome; smoking; human immunodeficiency virus deme
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                                                                                                                                                                                                                                                                  0 other;
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                                                                                                                                                comprising fragment of chemically modified and treatment of diseases associated with
                                                                                                                                                                                German
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Pred. No. 13;
0; Mismatches
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75.6%;
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2000DE-1043826
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Best Local Similarity
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                                                                                                                                   2002-130909/17
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2
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                                                                                                                                                  Nucleic acid c
for diagnosis
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01-SEP-2000;
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                 sapiens
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The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also relates to oligonucleotides or peptide nucleic acid (PNA) oligomers useful for detecting cytosine methylations. The pretreated DNA is useful for the diagnosis or therapy of behavioural disorders, neurological disorders, smoking, disorders and cancer, in particular major depressive disorder, Tourette's syndrome, schizophrenia, psychiatric and neurological disorders, smoking, drug abuse, alcoholism, personality traits, compulsive gambling, human immunodeficiency virus dementia, migraine, behaviours in schizophrenic and schizoaffective patients, and suicidal behaviour in patients with schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPs). The present sequence is human chemically treated genomic DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                     Novel nucleic acid useful for diagnosis and therapy of behavioral disorder, neurological disorder and cancer, comprises a sequence of segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G protein coupled receptor; cholecystokinin CCKB receptor;
rat; alpha-2A adrenergic receptor; human; screening; PCR primer;
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Pred. No. 13;
0; Mismatches 10; Indels
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                                                                                                                                                                        190pp; English
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Ozenberger BA;
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ilarity 75.6%;
Conservative 0
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SILVERMAN S.
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                                                                                                                                                                       Claim 1; Page 32-36;
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2002-154759/20.
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This is the DNA sequence of a primer that was used in the PCR amplification of DNA encoding the N-terminal portion (including 22 amino acids proximal to the 5th transmembrane domain) of rat cholecystokinin CCKB receptor, a G protein coupled receptor (GPCR). The PCR product was used in the construction of an intracellular loop 3 (IC3) deleted CCKB receptor mutant. Deletion of a portion of IC3 of mammalian GPCRs is correlated with improved functional expression in yeast cells with retention of full ability to couple to the heterotrimeric G protein. The invention relates to mutant GPCRs with constitutively activating mutations that permit the detection of the receptors' functional activity in the absence of activating ligands, host cells that contain mutations that promote the functional activity of the GPCRs, host cells expressing such receptors, and vectors useful for making such cells. The host cells receptors, in high the contain mutations for the functional activity of the GPCRs.
                          Novel host cells comprising heterologous G protein-coupled receptor modified to be constitutively active, useful for high throughput screening assays for e.g. drugs, insecticides or nematacides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New G protein-coupled receptors with a mutation in an intracell
domain, useful for high throughput screening assays for e.g. dr
insecticides or nematocides -
                                                                                                                                                                                                                                                                                                                            assays for therapeutic especially useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 36;
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r; drug screening; PCR primer;
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Pred. No. 28;
Mismatches (
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                                                                                                                                                                                                                                                                                                         receptors, and vectors useful for making are useful in high throughput screening insecticides, nematacides etc., and are
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24;
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                                                                                         75pp; English
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alpha 2A adrenergic receptor;
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larity 100.0%;
Conservative C
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 2000-246753/21
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                                                                                        Page
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36 BP;
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AAZ94369/c
ID AAZ94369 8
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Best Local S
Matches 24
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lular drugs,

English.

37pp;

16;

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Example

cells drugs,

Gaps

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This is the DNA sequence of a primer that was used in the PCR amplification of DNA encoding the N-terminal portion (including 39 amino acids proximal to the 5th transmembrane domain) of human alpha 2A adrenergic receptor, a G protein coupled receptor (GPCR).

The PCR product was used in the construction of an intracellular loop 3 (IC3) deleted receptor mutant. Deletion of a portion of a portion of IC3 of mammalian GPCRs is correlated with improved functional expression in yeast cells with retention of full ability to couple to the heterotrimeric G protein. The invention provides modified GPCRs having a mutation in IC3 that results in an improved functional response in cell-based assays. The modification promotes growth stimulation by a GPCR agonist, especially by improving coupling between the receptor and a heterotrimeric G protein. Polynucleotides encoding the mutated GPCR, chimeric GPCR, vectors and host cells are also claimed. The modified GPCRs can be used in improved high throughput screening assays (especially in yeast cells) for throughput screening assays (especially in yeast cells) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiinlergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; de
                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                            Length 37;
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28;
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100.0%;
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2000US-0180628.
2000US-0186464.
2000US-0186350.
2000US-0198123.
2000US-0198123.
2000US-0209467.
2000US-0214886.
2000US-0214886.
2000US-0216880.
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2000US-0217487.
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24; Conservative
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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Barash SC, Rosen CA,

WPI; 2001-541565/60

system antigen polypeptides treating nervous system nervous and/or t 3224 human diagnosing Nucleic acids encoding useful for preventing, cancers and metastases Nucleic acids useful for pre

SEQ ID NO 7495; 1701pp + Sequence Listing; English Disclosure;

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful the diagnosis, treatment and prevention of: (a) cancer, e.g. breast on other cancers of the adrenal gland, bone, bone and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; chaemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's colitis; (c) cardiovascular disorders such as myocardial ischaemias; colitis; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

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peroxisomal 3-oxoacyl-Coenzyme A thiolase; SNP; genotype; haple
single nucleotide polymorphism; polymorphic variant; enzyme; genosme.
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Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                       other;
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                                      4013 G; 3953
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/standard_name= "sing
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/*tag= 1
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/*tag= b
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/*tag= k
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/*tag= f
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/*tag= c
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replace (4157,T)
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/*tag= n
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replace(9182,A)
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ilarity 73.2%;
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Pred.
                                                           replace (15486,G)
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                            replace (15471, C)
/*tag= p
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/*tag= s
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/standard_name=
replace(14931,C)
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replace(18004,T)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
Human; acetyl-Coenzyme A acyltransferase; ACAA1; chromosome 3p23-p22;
peroxisomal 3-oxoacyl-Coenzyme A thiolase; SNP; genotype; haplotype;
single nucleotide polymorphism; polymorphic variant; enzyme; gene; ds
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Pred.
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73.28;
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DUDA A E.
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30; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymorphisms (SNP)
standard ambiguity
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                                                                                                                                                                           18-MAY-2000;
                                                              sapiens
                                                                                                                                                03-MAY-2001;
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ABQ47500
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Best Local
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(DUDA/)
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory of the central nervous, cardiovascular, gastrointestinal and respiratory of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                              The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders
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                                           2000DE-1043826
2000DE-1044543
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                                                                                           (EPIG-) EPIGENOMICS AG
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05-SEP-2000;
             01-SEP-2001;
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ABQ47501
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methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
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                                                                                                                                                                                                                                    method for determining the
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Pred. No. 52;
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77.8%;
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2000DE-1044543
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                                                                                                                                                                                                                                    invention
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01-SEP-2000;
05-SEP-2000;
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                                                                                                                                                                                         The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
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                                                                                                                  gene, useful
abnormal
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ent of diseases associated
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diseases. The present sequence
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ilarity 77.8%;
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          30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
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                                                                                                                                                                   Claim 1;
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The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also relates to oligonucleotides or peptide nucleic acid (PNA) oligomers useful for detecting cytosine methylations. The pretreated DNA is useful for the diagnosis or therapy of behavioural disorders, neurological disorders and cancer, in particular major depressive disorder, Tourette's syndrome, schizophrenia, psychiatric and neurological disorders, smoking, drug abuse, alcoholism, personality traits, compulsive gambling, human immunodeficiency virus dementia, migraine, behaviours in schizophrenic and schizoaffective patients, and suicidal behaviour in patients with schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPs). The present sequence is human chemically treated genomic DNA.
                                 Claim 1; Page 36-40; 190pp; English.
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Gaps ö Length 7353; Indels 8 1584 41 Score 23.2; D Pred. No. 52; 0; Mismatches 0; th 56.6%; Similarity 77.8%; 28; Conservative Query Match Best Local S Matches 28 1619 φ <del>a</del> ठे

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7353 BP; 1713 A; 384 C; 2140 G; 3116

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DB 24;

Search completed: March 10, 2003, 18:59:36 Job time : 56.9583 secs

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nucleic acid
DNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: douk
TOPOLOGY: linear
MOLECULE TYPE: DNA
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-9977-171-1
US-08-977-171-1
US-08-977-171-2
US-08-977-171-1
US-08-938-291A-2
US-08-804-227C-7
US-08-804-198-1
US-09-103-840A-2
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US-09-500-358-1
US-09-498-809-1
US-08-206-176-7
US-08-756-506-5
US-08-387-942C-31
US-08-188-228-49
US-08-332-643-43
US-08-332-643-49
US-08-35-638-49
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US-08-770-379-19
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US-08-136-993-6
Sequence 6, Application US/08136993
Patent No. 5420025
GENERAL INFORMATION:
APPLICANT: Takagi, Hiroshi
APPLICANT: Matsui, Hiroshi
APPLICANT: Matsui, Hiroshi
APPLICANT: Washizu, Kinya
APPLICANT: Washizu, Kinya
APPLICANT: Washizu, Kinya
APPLICANT: Koikeda, Satoshi
ITILE OF INVENTION: Recombinant tra
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Mi
STREET: 2100 Pennsylvania Avenue
CITY: N.W.
STREET: 2100 Pennsylvania Avenue
CITY: N.W.
STREET: 2037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,993
FILING DATE:
CLASSIFICATION: 1435
PRIOR
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/77,447

FILING DATE:
APPLICATION NUMBER: JP 2-282566
FILING DATE: 19-OCT-1990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-293-7060
TELEFAX: 202-293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 base pairs
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US-09-199-637A-131

is Sequence 131, Application US/09199637A

patent No. 6355411

igeneral INFORMATION:
APPLICANT: Ausubel, Frederick
APPLICANT: Rahme, Laurence G.
APPLICANT: Rahme, Laurence G.
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Wan-Wah
APPLICANT: Tan, Wan-Wah
APPLICANT: Tan, Wan-Wah
APPLICANT: Drenkard, Eliana
APPLICANT: Dre
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ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,993
FILING DATE:
CLASSIFICATION NUMBER: US/07/777,447
FILING DATE:
APPLICATION NUMBER: US/07/777,447
FILING DATE: 19-OCT-1990
TELEFOMMUNICATION INFORMATION:
TELEFOMMUNICATION INFORMATION:
TELEFAX: 202-293-7860
TELEFAX: 202-293-7860
TELEFAX: 1322-293-7860
TELEFAX: 202-293-7860
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US-08-136-993-12
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Avenue
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                       NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Z
STREET: 2100 Pennsylvania A
CITY: N.W.
STATE: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
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Similarity 75.0%;
27; Conservative
INVENTION:
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MOLECULE TYPE: l
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APPLICANT: Arafuka, Shino
APPLICANT: Matsui, Hiroshi
APPLICANT: Washizu, Kinya
APPLICANT: Washizu, Kinya
APPLICANT: Koikeda, Satoshi
TITLE OF INVENTION: Recombinant transglutaminase
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/77,447

FILING DATE: 19-OCT-1990

TELECOMMUNICATION INFORMATION:
TELEFAX: 202-293-7060

TELEFAX: 202-293-7860

TELEFAX: 202-293-7860

TELEX: 6491103

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSE: Sughrue, Mion, Zinn, Mac
STREET: 2100 Pennsylvania Avenue
CITY: N.W.
STATE: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
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Patent No. 5420025;
GENERAL INFORMATION:
APPLICANT: Takagi, Hiroshi
APPLICANT: Arafuka, Shino
APPLICANT: Matsui, Hiroshi
APPLICANT: Washizu, Kinya
APPLICANT: Washizu, Kinya
APPLICANT: Ando, Keiichi
APPLICANT: Koikeda, Satoshi
                                                                                                                                                                                                                                             Sequence 8, Application US/08136993
Patent No. 5420025
GENERAL INFORMATION:
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llarity 75.0%;
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EDNESS: double
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MOLECULE TYPE:
8-136-993-8
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US-08-136-993-12
                                                                                                                                                                                              RESULT 2
US-08-136-993-8
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F: Philippsen, Peter
F: Pohlmann, Rainer
F: Steiner, Sabine
F: Steiner, Sabine
F: Mohr, Christine
F: Wendland, Jurgen
F: Knechtle, Philipp
F: Knechtle, Philipp
F: Rebischung, Corinne
INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
INVENTION: AND USES THEREOF
                                                                           APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
TELEFAX: 919-541-8689
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                                                                                                                                                                                                                                  Corporation
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; Sequence 1040, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
                                                                                                                                                                                                                           ADDRESSEE: No. 6239264artis Carrest: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: No. 6239264artis
3054 Cornwallis Road
Steiner, Saccommon Mohr, Christine Wendland, Jurgen
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598 base pairs
nucleic acid
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MOLECULE TYPE: DNA (gen
ORIGINAL SOURCE:
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CORRESPONDENCE ADDRESS
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28; Conserv
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STREET: 3
CITY: Res
         APPLICANT:
APPLICANT:
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Best Local
Matches
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                                                                                                     Length 1436;
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US-08-700-626-2/C
Sequence 2, Application US/08700626
SEQUENCE 3.11 Man, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN DBI/ACBP-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
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Pred. No. 47;
0; Mismatches
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Pred. No.
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US-08-998-416-1090
; Sequence 1090, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
                                                                                                                                                                                                GGGCACCGAGCGCAGGCCCAACGGTCTGGGC
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Lucy J.
TER: 36,749
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,626
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:

; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-131

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larity 73.0%;
Conservative
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LENGTH: 1123 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LIBRARY: PGANNOT01
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COMPUTER READABLE |
MEDIUM TYPE: Di
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LIBRARY: Pur...
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US-08-700-626-2
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Best Local S
Matches 27
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Best Local
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APPLICANT: Sakut, Haim
APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: KOHN & ASSOCIATES
STREET: 30500 No. 6025183thwestern Highway, Suite 41
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suite
                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.30
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R: PF/5-30306/A/CGC1976
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Pred. No. 75;
0; Mismatches
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CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,099
                                                                                                                                                                                                                                                     FILLINCATION LINGER: 38,241
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-
TELEPHONE: 919-541-8587
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1040:
SEQUENCE CHARACTERISTICS:
LENGTH: 686 base pairs
TYPE: nucleic acid
TYPE: single
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Patent No. 6025183
GENERAL INFORMATION:
 6239264th Carolina
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Best Local Similarity 70.0%;
Matches 28; Conservative
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STATE: No. COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-998-416-1040
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US-08-814-095-7
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TELECOMMULICATION INPORANTION:
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TELECOMMULICATION:
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                                                        "arsenite resistance
OCATION: complement (34528..34895)
OTHER INFORMATION: /function= "arseniother information: /gene"
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /gene= "AR"
FEATURE:
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 5
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
                                                                                                                                                                                                                                                                 LOCATION: complement (33779..33963)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
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LOCATION: complement (32386..32468)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: complement (31363..31534)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
                                                                                                                                                                                                                                                                                                                                             NAME/KEY: exon
LOCATION: complement (33493..33591)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 4
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 11
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
                                                                                                                                                 NAME/KEY: exon
LOCATION: complement (34092..34358)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: complement (32569..32628)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 7
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/483,229
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 PLATELET AGGREGATION INHIBITORS
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Pred. No. 79;
0; Mismatches
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Pred. No. 1e+
0; Mismatches
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5318899-25/c
;Patent No. 5318899
; APPLICANT: SCARBOROUGH, ROBERT M.;WOLF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
5318899-27/c
;Patent No. 5318899
; APPLICANT: SCARBOROUGH, ROBERT M.;WOLF,
                                                            int (29664..29856)
/gene= "ARS"
/number= 16
  30073)
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07/483,229
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 418,028
FILING DATE: 06-OCT-1989
APPLICATION NUMBER: 367,509
FILING DATE: 16-JUN-1989
nt (29945..3
/gene= "AR"
/number= 15
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FILING DATE: 06-OCT-1989
APPLICATION NUMBER: 367,509
FILING DATE: 16-JUN-1989
SEQ ID NO:27:
LENGTH: 294
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ilarity 71.1%;
Conservative
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ilarity 74.3%;
Conservative
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larity 71.1%;
Conservative
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                                                               LOCATION: complement
OTHER INFORMATION: /
 LOCATION: complement
OTHER INFORMATION: //
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27; Conserv
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Best Local S
Matches 27
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Best Local S
Matches 26
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Best Local S
Matches 27
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Best Local
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, 90 South 7th
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r, 90 South 7th
RESULT 11
US-08-977-171-1/C

1 Sequence 1, Application US/08977171

2 Patent No. 6232112

3 GENERAL INFORMATION:

APPLICANT: CATCHESIDE, DAVID E.

TITLE OF INVENTION: REAGENTS AND METHODS FOR

TITLE OF INVENTION: OF DNA

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marchant, Gould, Smith, Edell, M

STREET: 3100 No. 6232112west Center, 90 Sou

CITY: Minneapolis

STREET: 3100 No. 6232112west Center, 90 Sou

CITY: Minneapolis

STREET: BANCANIN

COUNTRY: USA

ZIP: S5402

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/977,171

FILING DATE: 24-NOV-1997

CLASSIFICATION BATA:

APPLICATION DATA:

RICHING DATE:

FILING DATE:

ATTORNEY/AGENT

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Pred. No. 95;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 40,178
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
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t Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CATCHESIDE, DAVID E.
TITLE OF INVENTION: REAGENTS AND
TITLE OF INVENTION: OF DNA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smi
STREET: 3100 No. 6232112west Ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08977171
Patent No. 6232112
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 9775 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 71.1%;
Matches 27; Conservative
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NAME: Skoog, Mark T
REGISTRATION NUMBER: 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic DNA
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US-08-977-171-1
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CITY: Minne
STATE: MN
COUNTRY: US
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US-08-923-454A-17/c

Sequence 17, Application US/08923454A

Patent No. 6004794

GENERAL INFORMATION:

APPLICANT: Creasy, Caretha

APPLICANT: Livi, George

APPLICANT: Karran, Eric

APPLICANT: Clinkenbeard, Helen

APPLICANT: Southan, Christopher

TITLE OF INVENTION: HUMAN SERINE PROTEASE

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:
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STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2651 GGGCACCGCCGGCAAGCACGATGGACTCGGCCCCAACC
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,171
FILING DATE: 24-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
WINME: SKOOG, Mark T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCACCGAGGCCCAACGGTCTGGGCCCCGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20.4; D
Pred. No. 95;
0; Mismatches
                                                                                                                                                                                                                                             40,178
aR: 10552.13US01
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ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,4
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
                                                                                                                                                                                                                          NAME: Skoog, Mark T
REGISTRATION NUMBER: 40,178
REFERENCE/DOCKET NUMBER: 1055
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
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illarity 71.1%;
Conservative (
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TOPOLOGY: 1i
MOLECULE TYPE:
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CITY: Kis
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LOCATION: 13..42
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  NAME/KEY: misc feat
LOCATION: 13..42
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IMMEDIATE SOURCE:
CLONE: PBTA 74
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LOCATION:
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US-07-690-983D-17
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COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/690,983D
FILING DATE: 25-JUN-1991
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/AU90/00373
FILING DATE: 24-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                41
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Pred. No. 1.1e+02;
0; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                  190 GCGGCCAGCGCCCGGCTCGCAGCGGTCTGGGCACCCGGCG
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FILING DATE: 24-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/148 CF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/07690983D; Patent No. 5403586; GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, Gregory J. APPLICANT: STEWART, Andrew G. APPLICANT: TSONIS, Con G. TITLE OF INVENTION: FUSION PROTEINS; NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
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                                                                 17
                                                          INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
LENGTH: 2036 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                            th 49.3%;
Similarity 68.3%;
28; Conservative
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CLONE: pBTA 735
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; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORIGINAL SOURCE:
US-08-923-454A-17
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/note= "Coding sequence for LHRH
analogue"
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Pred. No. 1.7e+02;
); Mismatches 12
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FILING DATE: 25-JUN-
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU90/00373

FILING DATE: 24-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/148 CHI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/690,983D
FILING DATE: 25-JUN-1991
                                                                                                                                                                                                                                                                                                                         US-07-690-983D-27; Application US/07690983D; Patent No. 5403586; GENERAL INFORMATION: APPLICANT: RUSSELL-JONES, Gregory J. APPLICANT: STEWART, Andrew G. APPLICANT: TSONIS, Con G. TITLE OF INVENTION: FUSION PROTEINS; NUMBER OF SEQUENCES: 47; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
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Similarity 69.2%;
27; Conservative
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Query Match
Best Local Similarity 69.2%; Pred. No. 1.7e+02;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps
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Search completed: March 11, 2003, 07:41:04 Job time : 20.8886 secs

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RESULT 2
US-10-124-429-3
; Sequence 3, Application US/10124429
; Publication No. US20020187525A1
; GENERAL INFORMATION:
; APPLICANT: TAGUCHI, SEIICHI
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

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US-10-098-841-134
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  Sequence 1, Appli
Sequence 2, Appli
Sequence 3868, Ap
Sequence 9102, Ap
US-09-751-962-1
US-09-751-962-2
US-09-960-352-3868
US-09-864-761-9102
US-10-027-806-25
US-10-027-806-25
US-10-034-623-25
US-10-034-623-25
US-10-034-623-2
US-09-938-330-13
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US-09-938-330-15
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RESULT 1
US-09-983-965-4927
i Sequence 4927, Application US/09983965
j Patent No. US20020137160A1
j GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH
TILE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
CURRENT FILING DATE: 2001-10-26
FILE REFERENCE: 37-21 (1029)7
CCURRENT FILING DATE: 1999-12-17
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 5912
SEQ ID NO 4927
LENGTH 410
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US-09-975-719-131
is Sequence 131, Application US/09975719
is Publication No. US20030022349A1
is GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Rahme, Laurence G.
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361003
CURRENT FILING DATE: 2001-10-10
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 131
LENGTH: 1436
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Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
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Pred. No. 45;
0; Mismatches
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Pred. No. 52;
0; Mismatches
APPLICANT: MOMOSE, HARUO
TITLE OF INVENTION: A METHOD OF PRODUCING MI
FILE REFERENCE: 220567USOCONT
CURRENT APPLICATION NUMBER: US/10/124,429
CURRENT FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: PCT/JP00/07135
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3:1
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                                                                                                                                                                                                                                  ORGANISM: Streptoverticillium mobaraense
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Similarity 80.6%;
25; Conservative
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.0%;
Matches 27; Conservative
                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (578)..(1798)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-764-864-389/c
                                                                                                                                                                                 O ID NO 3
LENGTH: 1809
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Best Local S
Matches 25
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US-09-867-550-1483

US-09-867-550-1483

Sequence 1483, Application US/09867550

Patent No. US20020082206A1

GENERAL INFORMATION:

APPLICANT: Leach, Martin D.

APPLICANT: Conley, Pamela

APPLICANT: Law, Debbie

APPLICANT: Topper, James

TITLE OF INVENTION: No. US20020082206A1e1 Polynucleotides from Atherogenic Celli

TITLE OF INVENTION: Thereby

TITLE OF INVENTION: Thereby

FILE REFERENCE: 21402-013 (Cura-313)

CURRENT APPLICATION NUMBER: US/09/867,550

CURRENT FILING DATE: 2001-09-20

PRIOR APPLICATION NUMBER: USSN 60/208,427

PRIOR APPLICATION NUMBER: USSN 60/208,427

PRIOR FILING DATE: 2000-05-30

NUMBER OF SEQ ID NOS: 2125

SEQ ID NO 1483

LENGTH: 569
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Hillman, Jennifer L.
Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN DBI/ACBP-I
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Ir
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37
                                                                                                                                                                                                                 41
                                                                                                                                                Score 21; DB
Pred. No. 71;
0; Mismatches
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No.
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Pred.
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-859-101-2/c
; Sequence 2, Application US/09859101
; Patent No. US20020068825A1
; GENERAL INFORMATION:
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Prior application data removed
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 389
LENGTH: 514
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ilarity 73.0%;
Conservative (
                                                                                                                                               th 51.2%;
Similarity 73.0%;
27; Conservative
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US-09-867-550-1483
                                                                                                  ; ORGANISM: Homo sapiens
US-09-764-864-389
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27; Conserv
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Best Local S
Matches 27
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Best Local S
Matches 27
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                                                                                     TYPE: DNA
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US-10-098-841-134
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Matches
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APPLICANT: Xu, Chongjun
APPLICANT: Zhou, Ping
APPLICANT: Wang, Jian-Rui
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Jie
APPLICANT: Anng, Jie
APPLICANT: Chan, Xiaohong B.
APPLICANT: Ojan, Xiaohong B.
APPLICANT: Ojan, Xiaohong B.
APPLICANT: Ojan, Xiaohong B.
APPLICANT: Oran, Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1123;
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/859,101
FILING DATE: 14-May-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/700,626
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0115 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELEFAX: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21; DB
Pred. No. 71;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 784CIP2

CURRENT APPLICATION NUMBER: US/10/098,841

CURRENT FILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: 09/598,042

PRIOR FILING DATE: 2000-06-20

PRIOR FILING DATE: 2000-06-25

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 331

SOFTWARE: pt_FL_genes Version 1.0

SEQ ID NO 134

LENGTH: 1337

TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: PGANNOTO1
CLONE: 620984
;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-859-101-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 134, Application US/10098841 Publication No. US20020197679A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           LENGTH: 1123 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.2%;
ilarity 73.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang, Y. Tom
Liu, Chenghua
Asundi, Vinod
Xu, Chongjun
Zhou, Ping
Ma, Yunqing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
27; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -10-098-841-134/c
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Best Local S
Matches 27
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                 ö
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                ·;
                                                                                                                                                  Length 1337
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                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                    GGCACCGAGCCCAACGGTCTGGGCCCCGAGC
                                                                                                                                                                                                                                                                                  FILLE REFERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US/0180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2001-01-04

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                  Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09/608,408
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005849.1
                                                                                                                                                                                                                                                                                                                                                                               SSULT 8
3-09-864-761-5736/c
Sequence 5736, Application US/09864761
Patent No. US20020048763A1
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                                                                                                                                              51.2%;
illarity 73.0%;
Conservative
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JUMBER: US 6
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APPLICATION NUMBER: US
FILING DATE: 2000-09-21
APPLICATION NUMBER: US
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APPLICATION NUMBER:
FILING DATE: 2001-01
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (344)..(1192)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOS
                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION APPLICANT: Penn, S
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GGGGGCACCGAGGCCCAACGGTCTGGGCCCCGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(7521)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 28; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQ ID NO 3
LENGTH: 7521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-819-104A-3
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US-09-819-
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Matches
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US-10-006-950-1
; Sequence 1, Application US/10006950
; Patent No. US20020161216A1
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Bonini, James A.
; TITLE OF INVENTION: DNA ENCODING ORPHAN SNORF4 RECEPTOR
; FILE REFERENCE: 58799
; CURRENT APPLICATION NUMBER: US/10/006,950
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: US/09/266,407
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 2
cofTWARE: Patentin Ver. 2.0 - beta
                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                   Indels
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N PLACENTA, SIGNAL = 3.4
N LUNG, SIGNAL = 3.4
N FETAL LIVER, SIGNAL = 3.1
N ADULT LIVER, SIGNAL = 3.4
N HELA, SIGNAL = 3.4
N HEART, SIGNAL = 3.2
N BONE MARROW, SIGNAL =
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Pred. No. 82;
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0; Mismatches
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Pred. No. 84;
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TITLE OF INVENTION: Regulation of Human Lipox
TITLE OF INVENTION: Receptor-Like Protein
FILE REFERENCE: 4974.00453
CURRENT APPLICATION NUMBER: US/09/805,467A
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/189,037
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020058259A1
GENERAL INFORMATION:
APPLICANT: Ramakrishnan, Shyam
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Best Local Similarity 70.0
Matches 28; Conservative
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LENGTH: 2300
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US-09-819-104A-3/c

Sequence 3, Application US/09819104A

Publication No. US20030027137A1

GENERAL INFORMATION:

APPLICANT: Chen, J. Don

TITLE OF INVENTION:

TITLE OF INVENTION: AND USES THEREFOR

FILE REFERENCE: UMG-030

CURRENT APPLICATION NUMBER: US/09/819,104A

CURRENT FILING DATE: 2001-03-27

PRIOR APPLICATION NUMBER: 60/193,138

PRIOR FILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.0
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i Sequence 1, Application US/09819104A

j Sequence 1, Application US/09819104A

j Publication No. US20030027137A1

j GENERAL INFORMATION:

j APPLICANT: Chen, J. Don

j TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES

j TITLE OF INVENTION: AND USES THEREFOR

j FILE REFERENCE: UMG-030

j CURRENT APPLICATION NUMBER: US/09/819,104A

j CURRENT FILING DATE: 2001-03-27

j PRIOR PILING DATE: 2000-03-29

j NUMBER OF SEQ ID NOS: 6

j SOFTWARE: Patentin Ver. 2.0

j SEQ ID NO 1

j LENGTH: 8686
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Best Local Similarity 70.0%;
Matches 28; Conservative
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; FEATURE:
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; LOCATION: (157)..(7677)
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TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4787
LENGTH: 366
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                                                                                             CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult I
NUMBER OF SEQ ID NOS: 1198
SOFTWARE: PatentIn Ver. 2.0
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            Sequence 216, Application US/09764860 Patent No. US20020094953A1 GENERAL INFORMATION: APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, PERICE REFERENCE: PC008
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Rosen, Craig A.
Ruben, Steven M
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LOCATION: (198)
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US-09-783-590-4787
US-09-764-860-216
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OTHER INFORMATION: (Human Chromosome 11p15.5 PAC clone pDJ915f1
OTHER INFORMATION: containing KvLQT1 gene)
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; Sequence 6, Application US/10026188
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
; TITLE OF INVENTION: Ion Channel
; FILE REFERENCE: 02307E-114910US
; CURRENT APPLICATION NUMBER: US/10/026,188
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/259,379
; NUMBER OF SEQ ID NOS: 8
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Pred. No. 96;
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US-10-026-188-6
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Query Match Best Local Similarity 74.3%; Pred. No. 1e+02; Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Search completed: March 11, 2003, 23:15:29 Job time : 79.1538 secs

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## ALIGNMENTS

RESULT 1 BM967248/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	BM967248 ij32d04.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:6136374 5' similar to SW:A2AA_HUMAN P08913 ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence. BM967248.1 GI:19561047 EST.
ONGENI ON	nomo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
REFERENCE	1 to 561)
AUTHORS	<pre>Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,</pre>
	Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas M. Gibbons M. McCann R. Cole R. Tsagareishvili R. Williams T.
	Jackson, Y. and Bowers, Y.
TITLE JOURNAL	Endocrine Pancreas Consortium Unpublished (2000)
COPETENT	Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
	Tel: 617-495-1812

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/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
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                                                                                        on wrong strand
Email: dwelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA s
Washington University Genome Sequencing Center For
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 445.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6136374"
/clone_lib="Melton Normalized Human
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Pred. No. 2.8e-92;
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/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
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ij32c09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:6136336 5' similar to SW:AZAA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6136336"
/clone_lib="Melton Normalized Human Islet
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/dev_stage="Adult"
/lab_host="DH10B"
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Seq primer: -40RP from Gibco
High quality sequence stop: 455.
Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 691)
S Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
, Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagawi, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTE (Arakawa, T., et al. 2001)
L Unpublished (2001)
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Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-Tel: 81-45-503-9222
Fax: 81-45-503-9216
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N.,
Score 490.4;
Pred. No. 1.8e
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larity 99.8%;
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SOURCE
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adult male corpora
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Normalization and subtraction of cap-trapper-selected cDNAs to
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, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
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/db_xref="taxon:10090"
/clone="B230352011"
/clone_lib="RIKEN full-length enriched,
quadrigemina"
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 453)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Carden,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams
, Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
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Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing
Washington University Genome Sequencing Center This clone is
available royalty-free through LLNL; please contact the IMAGE
consortium (info@image.llnl.gov) for further information
Possible reversed clone: similarity on wrong strand
Location/Qualifiers
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AGTOGOGOGOTOAAAGCTCCCCCAAAACCTCTTCCTGGTGTCCCTGGCCTCAGCGGACATC
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ij34d05.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo cDNA clone IMAGE:6136736 5' similar to SW:A2AA_HUMAN P089ALPHA-2A ADRENERGIC RECEPTOR; mRNA sequence.
BQ129312.1 GI:20203223
EST.
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Divinity P
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Other ESTs: ij34d05.xl
Contact: Douglas Melton, Klaus H. Kaestner,
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Harvard University, Howard Hughes Medical
Dept of Molecular and Cellular Biology, 7
MA 02138
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/db_xref="taxon:9606"
/clone="IMAGE:6136736"
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/note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1; Site 2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this
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clone IMAGE:5266354 5
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 893)
NIH-MGC http://mgc.nci.nih.gov/.
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0; Mismatches 0
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                            /tissue_type="Islets
/dev_stage="Adult"
/lab_host="DH10B"
  lib="Melton
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TITLE
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                                                                                                                          ), Shiraki
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           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), & Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information car found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAMI1671 row: m column: 11
High quality sequence stop: 716.
Location/Qualifiers
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Pred. No. 6.1e-65;
0; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5266354"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
     Institutes of Health,
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Best Local Similarity 86.0%;
Matches 586; Conservative
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E 1 (bases 1 to 740)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11559 row: i column: 04

High quality sequence stop: 740.
                                                                                                                                                                                                                              BI838282
603083213F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222475 5',
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone=lib="LTI NFL006 PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: Not1; 1st strand cDNA
was primed with a Not1-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

84 a 397 c 385 g 168 t 3 others
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Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebr
Mammalia, Eutheria, Primates, Catarrhini, Homin

(bases 1 to 1077)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 364.8; DB 9;
Pred. No. 1.3e-56;
); Mismatches 152;
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chicken.
SM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianinae; Gallus.
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Submitted (14-SEP-2001) MRC Human Genome Mapping
Centre Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hgmp.mrc.ac.uk
Location/Qualifiers
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Pred. No. 1.6e-48;
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/organism="Gallus gallus'/db_xref="taxon:9031"
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1. 358
/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Ab xref="taxon:9606"
/ Clone_lib="HR85 islet"
/ Lissue_type="Purified pancreatic islet"
/ Lab host="DH10B"
/ Note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Not1; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                               MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 342.
Location/Qualifiers

1 358
              Homo sapiens

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 358)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas,
M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
Endocrine Pancreas Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Other ESTs: ig69h02.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Ir
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave,
MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
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TACGTCATCTCGTGCATCGGCTCCTTCTTCGCTCCCTGCCTCATCATGATCCTG
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/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
                                   867 bp mRNA linear EST 13-FEB-2001
prime, mRNA sequence.
AL530418
AL530418.1 GI:12793911
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Primates; Catarrhini; Hominidae; Homo
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Eukaryota; Metazoa; Chordata; Craniata; Vertebr
Mammalia; Eutheria; Primates; Catarrhini; Homin

(bases 1 to 867)

Li, w.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 317.6; DB 9;
Pred. No. 4.7e-48;
3; Mismatches 102;
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/clone_lib="LTI_NFL001_NBC4"
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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:6313133"
/clone=lib="NIH MGC 129"
/lab_host="DH10B (phage-resistant)"
/note="Organ: olfactory epithelium; Vector:
pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: Not1; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
unidirectionally. Primer: Oligo dT. Average insert size
is a NIH MGC Library."
is a NIH MGC Library."
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AGENCOURT_8764335 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313133
5', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 988)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Susan L. Sullivan, PhD.

Tissue Procurement: Susan L. Sullivan, PhD.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13739 row: m column: 06

High quality sequence start: 8

High quality sequence start: 8

High quality sequence stop: 509.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV0&t2=QV0-BT0263 101299-072-h10&t3=1999-12-10&t4=1)
Seq primer: puc 18 forward High quality sequence start: 26 High quality sequence stop: 205.

Location/Qualifiers
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1 (bases 1 to 297)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R. Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H. Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Shotgun sequencing of the home.
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/db_xref="taxon:9606"
/clone_lib="BT0263"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
Brazil
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Fax: +55-11-2707001
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Homo sapiens

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 935)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13611 row: b column: 15

High quality sequence stop: 535.

Location/Qualifiers

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Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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NotI; Site_2: SalI; cDNA made by
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AL236849.1 GI:7895984
GSS; genome survey sequence.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
E 1 (bases 1 to 896)
S Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCGG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size sele
1 kb for average insert length 1.87 kb. This is a process, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. college of Medicine) and is available through Life Technologies."
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., F.
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A.
Weissenbach, J.
Charaterization and repeat analysis of the compact genome freshwater pufferfish Tetraodon nigroviridis
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Submitted (12-APR-2000)
This sequence is a single read and was generated as part
scale clone-end sequencing project of the Tetraodon nigr
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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966 bp DNA linear GSS 14-MAY-2000
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AL205895
AL205895
AL205895.1 GI:7864714
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
Tetraodontidae; Tetraodon.
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Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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Human gene number estimate provided by genome wide analysis us Tetraodon nigroviridis DNA sequence
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Pred. No. 1.7e-31;
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Direct Submission

Submitted (12-APR-2000)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

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Pred. No. 2.4e-29;
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## ALIGNMENTS

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SEQ ID NO 1
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
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Pred. No. 8e-78;
0; Mismatches 422;
RESULT 1
US-10-077-870-1
; Sequence 1, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a r
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; CURRENT FILING DATE: 2002-05-21
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
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Best Local Similarity 62.4%;
Matches 820; Conservative (
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OTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 444.8; DB 10;
Pred. No. 8e-78;
0; Mismatches 422;
Sequence 1, Application US/09825923

Sequence 1, Application US/09825923

Patent No. US20010016338A1

GENERAL INFORMATION:

APPLICANT: Heinonen, Paula
APPLICANT: Alhopuro, Pia
APPLICANT: Karvonen, Matti
APPLICANT: Koulu, Markku
APPLICANT: Roulu, Markku
APPLICANT: Scheinin, Mika
APPLICANT: Scheinin, Mika
APPLICANT: Salonen, Ullamari
APPLICANT: Salonen, Tumo A
APPLICANT: Salonen, Timo A
APPLICANT: Salonen, Riitta
APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: Protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05

PRIOR FILLING DATE: 2000-05-25

MINNERS OF SEA
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SOFTWARE: Patentin Ver.
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APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a va
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                 CTGCCGCGCGCGGCGGGGGGACGGGGATCGGG
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Patent No. US20010016338A1
GENERAL INFORMATION:
APPLICANT: Snapir, Amir
APPLICANT: Heinonen, Paula
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Pesonen, Ullamari
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APPLICANT: Eunzow, James R.
APPLICANT: Bunzow, James R.
APPLICANT: Grandy, David K.
APPLICANT: Grandy, David K.
APPLICANT: Machida, Curtis A.
TITLE OF INVENTION: Dopamine Receptors and Ger
FILE REFERENCE: 90-1092-CCC
CURRENT APPLICATION NUMBER: 08/10/060,795B
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 08/474892
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1992-11-09
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1989-11-20
PRIOR FILING DATE: 1989-11-20
PRIOR FILING DATE: 1988-11-18
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Publication No. US20030040022A1
GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
RENT APPLICATION DATA:
APPLICATION NUMBER: US/09/349,755
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
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V: Muscarinic
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US-09-349-755-3
; Sequence 3, Application US/09349755
; Patent No. US20020166131A1
; GENERAL INFORMATION:
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NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & CO
STREET: 28 State Stree
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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TITLE OF INVENTION: Process for Identifyin
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
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Receptors and Uses Therefor
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Pred. No. 3.2e-24
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/166,334
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APPLICATION NUMBER: US 08/985,090
FILING DATE: 04-DEC-1997
ATTORNEY/AGENT INFORMATION:
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@QUENCES: 39
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Patent No. US20020168708A1
GENERAL INFORMATION:
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REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MN
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TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.4%;
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NUMBER OF SEQUENCES: 39
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CLASSIFICATION:
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APPLICATION NUMBER:
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Pred. No. 3.2e-24;
); Mismatches 410;
                                                                                                                                                      NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
COMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                        FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/985,090
FILING DATE: 04-DEC-1997
ATTORNEY/AGENT INFORMATION:
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US-09-349-755-3
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STRANDEDNESS: single
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; Patent No. US20020099199A1
; GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl a
; TITLE OF INVENTION: Muscarinic Re
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TENGTH: 1335 base pairs
compatible
PC-DOS/MS-DOS
In Release #1.0,
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EDNESS: single
COMPUTER: IBM PC compat
OPERATING SYSTEM: PC-DC
SOFTWARE: PatentIn Rele
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
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CLASSIFICATION:
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TITLE OF INVENTION: Muscarinic Receptors an
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
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APPLICATION NUMBER: US/09/042,780
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US 08/985,090
FILING DATE: 04-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
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Patent No. US20020166131A1
GENERAL INFORMATION:
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SEQUENCE DESCRIPTION: SEQ
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Patent No. US20020168708A1

GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses The
NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                             CGGCGCCCGGCCCACCCCTTACTCCCTGCAGGTGACGCTGACGCT
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ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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3.5e-24;
                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 168; DB
Pred. No. 3.5e.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
APPLICATION NUMBER: US 08/985,090
FILING DATE: 04-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/09/042,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/09/166,334
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nilarity 51.4%;
Conservative (
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                                    Massachusetts
. USA
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS 291
Boston
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US-09-166-334-1
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                                                                                      COUNTRY:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,206
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/444,783
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 151.8; DB 9;
Pred. No. 4.7e-21;
0; Mismatches 377;
                                                                             LLP
Americas
                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,991
FILING DATE: 28-Jun-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 178..1893
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                            DUNHAM
of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 391-052
          OF
     INVENTION: USE OF
                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                           EE: COOPER & 1185 Avenue
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                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                       NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS
ADDRESSEE: COOPER
                                                                                                                              STATE: New York COUNTRY: U.S.A.
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                                                                                                               New York
                                                                                                                                                                ZIP: 10036
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FEATURE:
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      TITLE
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Best Local S
Matches 432
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US-10-185-991-1
; Sequence 1, Application US/10185991
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; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski,
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APPLICANT: Weinshank et al, Richard L.
TITLE OF INVENTION: Method of Obtaining A Co; TITLE OF INVENTION: Selective Compound; FILE REFERENCE: 36536-BA; CURRENT APPLICATION NUMBER: US/10/005,010; CURRENT FILING DATE: 2001-10-29; PRIOR FILING DATE: 1999-08-09
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Sequence 3769, Application US/09864761
Sequence 3769, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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OR FILING DATE: 2000-02-04

OR APPLICATION NUMBER: US 60/207,456

OR APPLICATION NUMBER: US 09/632,366

OR FILING DATE: 2000-08-03

OR APPLICATION NUMBER: GB 24263.6

OR FILING DATE: 2000-10-04

OR APPLICATION NUMBER: US 60/236,359

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00667

OR APPLICATION NUMBER: PCT/US01/00667

OR APPLICATION NUMBER: PCT/US01/00667

OR APPLICATION NUMBER: PCT/US01/00669

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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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APPLICATION NUMBER: PCT/US01/00663
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Pred. No. 3.6e-20;
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
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PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine v
SEQ ID NO 3769
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 52.9%;
Matches 348; Conservative
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OTHER INFORMATION: MAD
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Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activit; phosphorylation; inositol phosphate; alpha-2AAR; GenBank Accession AF281308; chromosome 10; ds. "alpha-2AAR" Location/Qualifiers 1..1353 /\*tag= a /product= "alpha-2AA ВР encoding DNA 1350 entry) DNA; (first standard; alpha-2AAR WO200179561-A2 sapiens 17-APR-2001; 18-FEB-2002 5-OCT-2001 AAI99917; AA199917 Human Ношо Key

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The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising;

(a) obtaining a sample having a polymucleotide encoding an alpha-2B, alpha2A or alpha2C or fragment or complement of; and comprising cytosine or guanine at position 753 of (IIV)

of (I), a site comprising cytosine or guanine at position 753 of (IIV)

or a site comprising cytosine or guanine at position 753 of (IIV)

or a site comprising (A) (gggggggggcg) or (B) (ggggcggctgag) at positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2, comprising detecting a ssociated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In disease, central nervous system disease and combinations of these. Or alpha2A, or alpha2C agonist (e.g. epinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, combinations of these or antagonist (e.g. yohimbine, prazosin, ARC 239, chose) by detecting the polymorphic site and correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels, the present sequence is that of the human alpha-2AAR gene
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The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising;

(a) obtaining a sample having a polymucleotide encoding an alpha-2B, alpha2A or alpha2C or fragment or complement of; and

(b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I), a site comprising cytosine or guanine at position 753 of (IIV)

or a site comprising (A) (9999c999c9C9) or (B) (9999c99c9c9 at positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, compinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate cyclase, MAP kinase activity, phosphorylation or inositol phosphate
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the
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                                                                                                                                                             detecting cytosine methylation SEQ ID NO 34
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Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagn drug; side effect; cancer; central nervous system; cardiovascul gastrointestinal; respiratory system; single nucleotide polymor SNP; cell differentiation; ds. detecting cytosine methylation SEQ ID NO entry) ABQ47501 standard; DNA; Oligonucleotide for (first 12-JUL-2002 501 RESUL ABQ47

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01-SEP-2000; 2000DE-1043826 05-SEP-2000; 2000DE-1044543 2001WO-EP10074 WO200218632-A2 01-SEP-2001; Homo sapiens 07-MAR-2002 

Guetig 꾹 Berlin ບັ Piepenbrock WPI; 2002-371829/40 Olek A,

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(EPIG-) EPIGENOMICS

Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA + Sequence Listing; 56pp; German. 26pp Claim 12;

genomic of in This invention describes a novel method for determining the degree methylation of a particular cytosine in a motif 5'-CpG-3', present genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the geno

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DNA that contains the target C is amplified to form a labeled amplicon.

The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the rapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide systems etc., particularly by detecting mutations of call or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the invention.
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated two classes, each with at least one cand the degree of hybridisation to both classes is determined from the amoticon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the cancer, particularly by detecting mutations or single nucleotide systems etc., particularly by detecting mutations or single nucleotide systems etc., particularly by detecting mutations of cell or tissue types and for investigating cell differentiation of cell or tissue methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention. disorders method

56pp; German

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Claim 12; 56pp

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ô The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also relates to oligonucleotides or peptide nucleic acid (PNA) oligomers useful for detecting cytosine methylations. The pretreated DNA is useful for the diagnosis or therapy of behavioural disorders, neurological disorders, and cancer, in particular major depressive disorders, smoking, disorders and cancer, in particular major depressive disorders, smoking, drug abuse, alcoholism, personality traits, compulsive gambling, human immunodeficiency virus dementia, migraine, behaviours in schizophrenic and schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPs). The present sequence is human chemically treated genomic DNA. Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism; behavioural disorder; neurological; psychiatric; cancer; schizophrenia; Tourette's syndrome; smoking; human immunodeficiency virus dementia; 6320 Ø Novel nucleic acid useful for diagnosis and therapy of behavioral disorder, neurological disorder and cancer, comprises a sequence of segment of chemically pretreated DNA of adrenergic alpha-1C-receptor Gaps 9 TTGAACCCCGGTCATCTACACCATCTTCAACCACGATTTCCGCCGCGCGCTTCAAGAAGATC ATGGGCTCCCTGCAGCCGGACGCGAACGCGAAGCTGGAACGGGACCGAGGCGCGGGG ö Length 7353 0 other; Indels ; DB 24; 2.9e-123; thes 320; Ħ, C; 1956 G; 3469 d. No. 2.9 Mismatches #3. 62.1%; Score 838; larity 76.3%; Pred. No. 2 Conservative 0; Mismatch treated genomic DNA CTCTGTCGGGGGGACAGGAAGCGGATCGTG TTTTGTCGGGGGATAGGAAGCGGATCGTG English Berlin ·; BP; 1544 A; 384 32-36; 190pp; 2001WO-EP07540 2000DE-1032529 2000DE-1043826 entry) ds DNA; ΰ migraine; Piepenbrock (first EPIGENOMICS 2002-154759/20 standard; Query Match Best Local Similarity Matches 1030; Conser chemically WO200202809-A2 Claim 1; Page 7353 30-JUN-2000; 01-SEP-2000; 02-JUL-2001; abuse; -APR-2002 10-JAN-2002 AAD28362; AAD28362 Sequence (EPIG-) Ä 6321 drug 6261 WPI; 1261 Olek RESULT 10 gene 5001 H AAD28362 g ò Π

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"sequence includes a 12 nucleotide polymorphic
site at nucleotides 961-972 absent in the
alpha-2CAR variant (AAI99933)"
                                                                                                                                                                                                                                                                                               Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity phosphorylation; inositol phosphate; alpha-2CAR; chromosome 4; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a) obtaining a sample having a polynucleotide encoding an alpha-2B, alpha2A or alpha2C or fragment or complement of; and (b) detecting a polymorphic site comprising nucleotide positions 901 of (I), a site comprising cytosine or guanine at position 753 of (II) or a site comprising (A) (ggggcgggccg) or (B) (ggggcggctgag) at
                                                                                              TGCTCCGTGCCACGCACGCTCTTCAAATTCTTCTTCTGGTTCGGCTACTGCAACAGCTCG
                                               TTGAACCCGGTCATCTACACCATCTTCAACCACGATTTCCGCCGCGCCTTCAAGAAGATC
Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene us
determining whether an individual is at increased risk of dev
disease associated with the corresponding receptor comprises
a polymorphic site -
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positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, combinations of these) or antagonist (e.g. epinephrine, prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the human alpha-2CAR, the sequence includes a 12 nucleotide polymorphic site at nucleotides sequence in the alpha-2CAR variant (AA199933).
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C; 500 G; 237 T; 0 other; 482 Sequence 1383 BP; 164 A;

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1..1371
/*tag= a
/product= "alpha-2CAR"
/note= "sequence is deleted for a 12 nucleotide
/note= polymorphic site at nucleotides 961-972
wildtype sequence (AAI99931)"
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                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (1)-(III) by detecting a polymorphic site, comprising; (a) obtaining a sample having a polymorphic site, comprising; (b) detecting a polymorphic site comprising an alpha-2B, alpha2A or alpha2C or fragment or complement of; and cerecting a polymorphic site comprising net position 753 of (IIV) or a site comprising (A) (ggggcggggccg) or (B) (ggggcgggctgag) at alpha2A, and pha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, clonidine, oxymeteracoline, guanababaz, uKA1304, BHT933 and combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and combinations of these) or antagonist site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate clevels). The present sequence is that of the human alpha-2CAR variant, the sequence is deleted for a 12 nucleotide polymorphic site at the response correlating the correlation.
                                                                                                                                                                                                                                                                1-2B, 2A, or 2C adrenergic receptor gene useful for an individual is at increased risk of developing a with the corresponding receptor comprises detecting
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/*tag= a
/product= "alpha-2BAR"
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10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
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P-PSDB; AAM52118.
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receptor gene (I)-(III) by detecting a polymorphic site, comprising;

(a) obtaining a sample having a polymucleotide encoding an alpha-2B,

alpha2A or alpha2C or fragment or complement of; and

(b) detecting a polymorphic site comprising nucleotide position 901-909

of (I), a site comprising Cytosine or guanine at position 753 of (IIV)

or a site comprising (A) (ggggcgggccg) or (B) (ggggcggctggg) at

CC or a site comprising (A) (gggcggggccg) or (B) (ggggcggctggg) at

obsitions 961-972 of (III). The method may be used for genotyping an

cc alpha2B, alpha2A or alpha2C receptor gene and further used to determine

whether an individual is at increased risk of developing a disease

comprising site which correlate to disease selected from cardiovascular

colymorphic site which correlate to disease selected from cardiovascular

disease, central nervous system disease and combinations of these. In

addition, the technique may be used to predict an individual's response

contained alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,

combinations of these) or alpha2C agonist (e.g. epinephrine,

combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,

crauwolscine, idazoxan, tolazoline, phentolamine and combinations of

these) by detecting the polymorphic site and correlating the site to a

cyclase, MAP kinase activity, phosphorylation or inositol phosphate

clevels). The present sequence is that of the third intracellular loop of

the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide

colymorphic site found at nucleotides 901-909 of the wildype gene
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Pred. No. 1.9e-61;
); Mismatches 406;
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Best Local Similarity 63.4%;
Matches 834; Conservative
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STREET: Eleventh FLOCE,
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DECOMPATIBLE FORM:
MEDIUM TYPE: PATENTIN RElease #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/676,174A
FILING DATE: 19910328
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOLT, WALSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/79117/KIK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)861-3000
TELEFAX: (202)82-8944
TELEFAX: (202)82-8944
TELEFX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
US-08-461-812-1

US-08-087-772A-14

US-08-08-01-1

US-08-450-962-1

US-08-056-051-5

US-07-928-611-21

US-09-378-074-21

US-08-313-553-8

US-08-313-553-8

US-08-767-993-8

US-08-767-993-8

US-08-767-993-8

US-08-767-993-8

US-08-767-993-8

US-08-767-993-8

US-08-767-993-8

US-08-767-993-8
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Pred. No. 2.8e-23
; Mismatches 26
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                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                               RESULT 1
US-07-676-174A-1
; Sequence 1, Application US/07676174A
; Patent No. 5344776
; GENERAL INFORMATION:
; APPLICANT: Ventor, J. Craig
TITLE OF INVENTION: Octopamine rec;
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSH
; STREET: Eleventh Floor, 1615 L.
; CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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il Similarity 56.2%;
352; Conservative
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LENGTH: 3335 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
     319
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LOCATION:
7-676-174A-1
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REFERENCE/DOCKET NUMBER: MNI-032
TELECOMMUNICATION INFORMATION:
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TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                              12.4%;
iilarity 51.4%;
Conservative
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3: cDNA
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Best Local Similarity
Matches 440; Conser
                                                                                                                                                                                                   TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
S-08-985-090-3
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Floppy disk
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NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATI
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                                                                                                              APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/165,543
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Pred. No.
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                                                                               Sequence 3, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
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NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CITY: BC
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US-09-165-543-3
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC REINUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD,
STREET: 28 State Street
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Pred. No. 3.2e-2;
); Mismatches 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2689 base pairs
                                                                                                                                                                                                                               STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
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                                                                                                                                                                  APPLICANT: Andrew D.J. Goodearl a TITLE OF INVENTION: Muscarinic ReNUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD, STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                      RESULT 5
US-09-165-543-1
; Sequence 1, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
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US-09-642-855-6
; Sequence 6, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: SUBTYPE
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CURRENT APPLICATION NUMBER: US/09/167,354A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Lovenberg, Timothy
APPLICANT: Erlander, Mark
APPLICANT: Pyati, Jayashree
APPLICANT: Huvar, Arne
TITLE OF INVENTION: DNA ENCODING A HUR
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US-09-642-514-6

Sequence 6, Application US/09642514

Patent No. 6437100

GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Erlander, Mark
APPLICANT: Pyati, Jayashree
APPLICANT: Pyati, Jayashree
TITLE OF INVENTION: DNA ENCODING A HUMAN HIS
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: ORT1290
CURRENT APPLICATION NUMBER: US/09/642,514
CURRENT FILING DATE: 2000-08-21
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: 09/167,354
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
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; Sequence 5, Application US/0964285
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING
; TITLE OF INVENTION: SUBTYPE
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SUBTYPE
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APPLICANT: Lovenberg, Timothy
APPLICANT: Erlander, Mark
APPLICANT: Pyati, Jayashree;
APPLICANT: Huvar, Arne
TITLE OF INVENTION: DNA ENCODING A HUMAN
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: ORT1290
CURRENT APPLICATION NUMBER: US/09/642,514
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Patent No. 5556753
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                         Sequence 15, Application US/08475742; Patent No. 6121015; GENERAL INFORMATION:
APPLICANT: O'Malley, Karen L
APPLICANT: Todd, Richard D
TITLE OF INVENTION: Gene Encoding the Ra
FILE REFERENCE: WU 102 CON DIV
CURRENT APPLICATION NUMBER: US/08/475,74
CURRENT FILING DATE: 1995-06-07
EARLIER FILING DATE: 1994-06-16
EARLIER FILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIN Ver. 2.0
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NAME/KEY: misc_feature
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PUBLICATION INFORMATION:
TITLE: Cloning and expression of TITLE: cDNA.
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Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Ad-
TITLE OF INVENTION: Receptors and Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
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932
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.24
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4187
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08228932
Patent No. 5578611
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      SEE: COOPER & DUNHAM
: 30 Rockefeller Plaza
New York
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Best Local Similarity 51.9%;
Matches 432; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis
COMPUTER: IBM PC compat
OPERATING SYSTEM: PC-DC
SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 13-APR-199
CLASSIFICATION: 514
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SS: single
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Charles G
APPLICANT: Theresa A
TITLE OF INVENTION:
TITLE OF INVENTION:
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RY: U.S.A.
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APPLICANT:
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CITY: Na
STATE: 1
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US-08-228-932-1
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Pred. No. 2.6e-19;
0; Mismatches 377;
                                                US/08/334,698
                                                                                                   US/07/952,798
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,698
                                                                                                                                                  28,678
37690I
                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/952,
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 3769(
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 977-9550
TELEFAX: (212) 664-0525
TELEFAX: (212) 664-0525
TELEFAX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
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nilarity 51.9%;
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; OTHER INFORMATION:
US-08-334-698-1
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432; Conser
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Best Local S
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A. Branchek, John M. Wetzel and Paul R. Hartig
USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
PROSTATIC HYPERPLASIA
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Pred. No. 2.6e-19;
); Mismatches 377;
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APPLICANT: Jonathan A. Bard et al.

TITLE OF INVENTION: DNA Encoding Human Al

TITLE OF INVENTION: Receptors and Uses Th

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: COOPER & DUNHAM LLP

STREET: 1185 Avenue of the Americas
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
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Pred. No. 2.
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,939
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                  41337-1B
                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4133
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                          TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ilarity 51.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: 178.1893
; OTHER INFORMATION:
US-08-468-939-1
FORM:
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432; Conserv
COMPUTER READABLE
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ANTI-SENSE:
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Search completed: March 11, 2003, 07:41:17 Job time : 108.111 secs